Amendments to the Specification

On page 4, please replace the paragraph starting on line 33 with the following:

The regulated transcriptional regulatory region in the selectable marker expression cassette is one which expresses in transformed callus cells at a significantly higher level than in the selected target tissue, e.g., seeds, and hybridizes under conditions of high stringency with the rice ~~alpha-glucanase~~beta-glucanase gene promoter Gns-9 identified by SEQ ID NO:1. The promoter may be contained in the sequence identified by SEQ ID NO:1.

On page 5, please replace the paragraph starting on line 30 with the following:

In still another aspect, the invention includes a plant transformation expression cassette for transforming monocot plant cells with a selectable marker gene containing, operatively linked in sequence in a 5' to 3' direction, (i) a transcriptional regulatory region which hybridizes under high-stringency conditions with a rice ~~alpha-glucanase~~beta-glucanase gene promoter identified by SEQ ID NO:1, and which expresses in callus cells at a significantly higher level than in a selected target tissue, (ii) a selectable marker gene, and (iii) a 3' untranslated terminator region.

On page 8, please replace the paragraph starting on line 24 with the following:

"Heterologous DNA" or "foreign DNA" refers to DNA, and typically to a DNA coding sequence ("heterologous coding sequence"), which has been introduced into plant cells from another source, that is, a non-plant source or from another species of plants, or a same-species coding sequence which is placed under the control of a plant promoter that normally controls another coding sequence. An insulin coding sequence placed under the control of a plant promoter is an example of a heterologous DNA, as is a rice alpha-glucanase or beta-glucanase coding sequence placed under the control of a barley α-amylase promoter.

On page 9, please replace the paragraph starting on line 13 with the following:

A DNA sequence is "derived from" a gene, such as a rice alpha-glucanase or beta-glucanase gene, if it corresponds in sequence to a segment or region of that gene. Segments of genes which may be derived from a gene include the promoter region, the 5' untranslated region, and the 3' untranslated region of the gene.

On page 11, please replace the paragraph starting on line 6 with the following:

The transcriptional regulatory region, or promoter, is a regulated promoter which expresses in callus tissue at significantly higher levels than in selected target plant tissue. One preferred promoter is the rice ~~alpha-glucanase-9~~beta-glucanase-9 (Gns9) promoter. The Gns9 promoter, together with several other rice alpha-glucanase or beta-glucanase promoters, have been described in U.S. patent application SN 09/105,390, filed June 25, 1998, which is incorporated by reference.

On page 20, please replace the paragraph starting on line 26 with the following:

An exemplary selectable marker vector was constructed in three steps. First, a DNA fragment was amplified from the rice alpha-amylase gene, RAmy1A, (Huang N. *et al.* (1990) Plant Molecular Biology 14: 655-668), using the primers 1AR1: 5' AAC AAT ACT GGA ATT CGA GAA GTA AAA AG 3' (SEQ ID NO:[[3]]5) and 1ASma: 5' CTA CGC AAC CCG GGA GAA AAT C 3' (SEQ ID NO:[[4]]6). The amplified fragment, containing 297 bp of the RAmy1A terminator, was cloned into the SmaI/EcoRI restriction sites of pBluscript KS+, resulting in plasmid p1AT. Second, a BamHI DNA fragment from plasmid pGL2 (Shimamoto *et al.* (1989) Nature 338: 274-276) encoding hygromycin phosphotransferase (HPH) was cloned into the BamHI site of p1AT, resulting in plasmid pAPI74. The pGL2 BamH1 fragment encodes the full-length HPH polypeptide sequence minus four C-terminal amino acids. Third, a SacI/XbaI fragment was amplified from rice ~~alpha-glucanase~~beta-glucanase gene Gns9 using the primers gnsF, 5' GAC TTA ACT TTA GTC ATA TTT AG 3' (SEQ ID NO:[[5]]7) and GnsR 5' TTC GCT CTT GCT GCT GCT CACT 3'(SEQ ID NO:[[6]]8) and was inserted into the SacI/XbaI sites of pAPI74 to form pAPI76. The sequence of all fragments was confirmed by DNA sequencing.

On page 21, please replace the paragraph starting on line 13 with the following:

First, the extra ATG near the translational start codon was removed by site-directed mutagenesis (SDM), and for cloning purpose, a BamHI site was changed to BglII sites at the same time. Two site specific ~~mutangenesis~~mutagenesis primers are synthesized:

API Primer #110 - Hph-SDM1

BamHI (pAPI 76)

GGATCC T

GCAGTCTAGAACTAGTAGATCTCGGGGGGCAACGAAATATGAAAAAGCC (SEQ ID NO: 9)

BglII

API Primer #109 Hph-SDM2

GGCTTTTTCATATTTCGTTGCCCCCCGAGATCTACTAGTTCTAGACTGC (SEQ ID NO: 10)

On page 21, please replace the paragraph starting on line 24 with the following:

The mutagenesis was done by using PCR and Quick Change Kit from Stratgene, CA. The resulting plasmid is called pAPI76(SDM). To repair the C-terminus of pAPI76(SDM), the following two primers were synthesized in order to generate a PCR fragment:

API Primer #111 - Hph-Rev

E K A R

T AAT GGA TCC TCA TTC CTA TTC CTT TGC CCT CGG ACG AGT GCT GGG G (SEQ ID NO: 11)

BamHI stop stop

API Primer #114 - Hph-fwd

ATCGCCGCGGCTCCGGGCGTATATGC (SEQ ID NO: 12)

SacII

On page 21, please replace the paragraph starting on line 35 with the following:

The PCR fragment that was generated with the two primers, using pAPI76 as a template, was digested with SacII and BamHI and inserted into pAPI76(SDM) which as been cut with SacII/BamHI. The resulting plasmid is called pAPI106. DNA sequencing confirmed the correct site directed ~~mutangenesis~~mutagenesis.

On page 22, please replace the paragraph starting on line 13 with the following:

Primer-1 (KANF1) begins 146 nt upstream of the ATG for the kan^r gene and primer-2 (KANR1) ends 19 nt downstream of the stop codon for the same gene.

*Ssp*I half site

Primer-1 = KanF1 5'- ATTGCAAGCGAACCGGAATTGCCAG -3' (SEQ ID NO: 13)

*Dra*I half site

Primer-2 = KanR1 5'- AAACTCTTCCTTTTTCAATTCAG -3' (SEQ ID NO: 14).